

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 09/517, 491 B
Source: JFW16
Date Processed by STIC: 07/26/2005

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 07/26/2005

PATENT APPLICATION: US/09/517,491B

TIME: 12:41:58

Input Set : A:\ABPI-P06-036.TXT

Output Set: N:\CRF4\07262005\I517491B.raw

(pg-6)

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4 <110> APPLICANT: Berlin, Vivian
5      Chiu, Maria Isabel
6      Cottarel, Guillaume
7      Damagnez, Veronique
9 <120> TITLE OF INVENTION: IMMUNOSUPPRESSANT TARGET PROTEINS
12 <130> FILE REFERENCE: APBI-P06-036
14 <140> CURRENT APPLICATION NUMBER: US 09/517,491B
15 <141> CURRENT FILING DATE: 2000-03-02
17 <150> PRIOR APPLICATION NUMBER: US 08/360,144
18 <151> PRIOR FILING DATE: 1994-12-20
20 <150> PRIOR APPLICATION NUMBER: US 08/250,795
21 <151> PRIOR FILING DATE: 1994-05-27
23 <160> NUMBER OF SEQ ID NOS: 35
25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 486
29 <212> TYPE: DNA
30 <213> ORGANISM: Mouse
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (1)...(486)
36 <400> SEQUENCE: 1
37 ctc acc cgt cac aat gca gcc aac aag atc ttg aag aac atg tgt gaa 48
38 Leu Thr Arg His Asn Ala Ala Asn Lys Ile Leu Lys Asn Met Cys Glu
39 1 5 10 15
41 cac agc aac acg ctg gtc cag cag gcc atg atg gtg agt gaa gag ctg 96
42 His Ser Asn Thr Leu Val Gln Gln Ala Met Met Val Ser Glu Glu Leu
43 20 25 30
45 att cgg gta gcc atc ctc tgg cat gag atg tgg cat gaa ggc ctg gaa 144
46 Ile Arg Val Ala Ile Leu Trp His Glu Met Trp His Glu Gly Leu Glu
47 35 40 45
49 gag gca tct cgc ttg tac ttt ggg gag agg aac gtg aaa ggc atg ttt 192
50 Glu Ala Ser Arg Leu Tyr Phe Gly Glu Arg Asn Val Lys Gly Met Phe
51 50 55 60
53 gag gtg ctg gag ccc ctg cat gct atg atg gaa cgg ggt ccc cgg act 240
54 Glu Val Leu Glu Pro Leu His Ala Met Met Glu Arg Gly Pro Arg Thr
55 65 70 75 80
57 ctg aag gaa aca tcc ttt aat cag gca tat ggc cga gat tta atg gag 288
58 Leu Lys Glu Thr Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu
59 85 90 95
61 gca caa gaa tgg tgt cga aag tac atg aag tcg ggg aac gtc aag gac 336
62 Ala Gln Glu Trp Cys Arg Lys Tyr Met Lys Ser Gly Asn Val Lys Asp
63 100 105 110

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65 ctc acg caa gcc tgg gac ctc tac tat cac gtg ttc aga cgg atc tca 384
66 Leu Thr Gln Ala Trp Asp Leu Tyr Tyr His Val Phe Arg Arg Ile Ser
67      115      120      125
69 aag cag cta ccc cag ctc aca tcc ctg gag ctg cag tat gtg tcc ccc 432
70 Lys Gln Leu Pro Gln Leu Thr Ser Leu Glu Leu Gln Tyr Val Ser Pro
71      130      135      140
73 aaa ctt ctg atg tgc cga gac ctt gag ttg gct gtg cca gga aca tac 480
74 Lys Leu Leu Met Cys Arg Asp Leu Glu Leu Ala Val Pro Gly Thr Tyr
75 145      150      155      160
77 gac ccc 486
78 Asp Pro
82 <210> SEQ ID NO: 2
83 <211> LENGTH: 162
84 <212> TYPE: PRT
85 <213> ORGANISM: Mouse
87 <400> SEQUENCE: 2
88 Leu Thr Arg His Asn Ala Ala Asn Lys Ile Leu Lys Asn Met Cys Glu
89 1      5      10      15
90 His Ser Asn Thr Leu Val Gln Gln Ala Met Met Val Ser Glu Glu Leu
91      20      25      30
92 Ile Arg Val Ala Ile Leu Trp His Glu Met Trp His Glu Gly Leu Glu
93      35      40      45
94 Glu Ala Ser Arg Leu Tyr Phe Gly Glu Arg Asn Val Lys Gly Met Phe
95      50      55      60
96 Glu Val Leu Glu Pro Leu His Ala Met Met Glu Arg Gly Pro Arg Thr
97 65      70      75      80
98 Leu Lys Glu Thr Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu
99      85      90      95
100 Ala Gln Glu Trp Cys Arg Lys Tyr Met Lys Ser Gly Asn Val Lys Asp
101      100      105      110
102 Leu Thr Gln Ala Trp Asp Leu Tyr Tyr His Val Phe Arg Arg Ile Ser
103      115      120      125
104 Lys Gln Leu Pro Gln Leu Thr Ser Leu Glu Leu Gln Tyr Val Ser Pro
105      130      135      140
106 Lys Leu Leu Met Cys Arg Asp Leu Glu Leu Ala Val Pro Gly Thr Tyr
107 145      150      155      160
108 Asp Pro
112 <210> SEQ ID NO: 3
113 <211> LENGTH: 40
114 <212> TYPE: DNA
115 <213> ORGANISM: Artificial Sequence
117 <220> FEATURE:
118 <223> OTHER INFORMATION: oligonucleotide
120 <400> SEQUENCE: 3
121 gggtttggaa ttcttaataa tgtctgtaca agtagaaacc 40
123 <210> SEQ ID NO: 4
124 <211> LENGTH: 34
125 <212> TYPE: DNA
126 <213> ORGANISM: Artificial Sequence

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128 <220> FEATURE:
129 <223> OTHER INFORMATION: oligonucleotide
131 <400> SEQUENCE: 4
132 ggggtttcggg atccccgtcat tccagtttta gaac 34
134 <210> SEQ ID NO: 5
135 <211> LENGTH: 348
136 <212> TYPE: DNA
137 <213> ORGANISM: Homo sapiens
139 <220> FEATURE:
140 <221> NAME/KEY: CDS
141 <222> LOCATION: (14)...(325)
143 <400> SEQUENCE: 5
144 ggaattccta ata atg tcc gta caa gta gaa acc atc tcc cca gga gac 49
145 Met Ser Val Gln Val Glu Thr Ile Ser Pro Gly Asp
146 1 5 10
148 ggg cgc acc ttc ccc aag cgc ggc cag acc tgc gtg gtg cac tac acc 97
149 Gly Arg Thr Phe Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr
150 15 20 25
152 ggg atg ctt gaa gat gga aag aaa ttt gat tcc tcc cgt gac cgt aac 145
153 Gly Met Leu Glu Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn
154 30 35 40
156 aag ccc ttt aag ttt atg cta ggc aag cag gag gtg atc cga ggc tgg 193
157 Lys Pro Phe Lys Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp
158 45 50 55 60
160 gaa gaa ggg gtt gcc cag atg agt gtg ggt cag cgt gcc aaa ctg act 241
161 Glu Glu Gly Val Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr
162 65 70 75
164 ata tct cca gat tat gcc tat ggt gcc act ggg cac cca ggc atc atc 289
165 Ile Ser Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile
166 80 85 90
168 cca cca cat gcc act ctc gtc ttc gat gtg gag ctt ctaaaactgg 335
169 Pro Pro His Ala Thr Leu Val Phe Asp Val Glu Leu
170 95 100
172 aatgacggga tcc 348
174 <210> SEQ ID NO: 6
175 <211> LENGTH: 104
176 <212> TYPE: PRT
177 <213> ORGANISM: Homo sapiens
179 <400> SEQUENCE: 6
180 Met Ser Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
181 1 5 10 15
182 Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
183 20 25 30
184 Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
185 35 40 45
186 Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
187 50 55 60
188 Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
189 65 70 75 80

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190 Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
191          85                      90                      95
192 Thr Leu Val Phe Asp Val Glu Leu
193          100
196 <210> SEQ ID NO: 7
197 <211> LENGTH: 48
198 <212> TYPE: DNA
199 <213> ORGANISM: Artificial Sequence
201 <220> FEATURE:
202 <223> OTHER INFORMATION: oligonucleotide
204 <400> SEQUENCE: 7
205 tcgccggaat tcgggggcgg aggtggagga gtacaagtag aaaccatc      48
207 <210> SEQ ID NO: 8
208 <211> LENGTH: 34
209 <212> TYPE: DNA
210 <213> ORGANISM: Artificial Sequence
212 <220> FEATURE:
213 <223> OTHER INFORMATION: oligonucleotide
215 <400> SEQUENCE: 8
216 gggttttcggg atcccgatcat tccagtttta gaag      34
218 <210> SEQ ID NO: 9
219 <211> LENGTH: 41
220 <212> TYPE: DNA
221 <213> ORGANISM: Artificial Sequence
223 <220> FEATURE:
224 <223> OTHER INFORMATION: oligonucleotide
226 <400> SEQUENCE: 9
227 cgcggatccg cgcattatta cttgttttga ttgatttttt g      41
229 <210> SEQ ID NO: 10
230 <211> LENGTH: 40
231 <212> TYPE: DNA
232 <213> ORGANISM: Artificial Sequence
234 <220> FEATURE:
235 <223> OTHER INFORMATION: oligonucleotide
237 <400> SEQUENCE: 10
238 cgcggatccg cgtaaaagca aagtactatc aattgagccg      40
240 <210> SEQ ID NO: 11
241 <211> LENGTH: 5430
242 <212> TYPE: DNA
243 <213> ORGANISM: Homo sapiens
245 <220> FEATURE:
246 <221> NAME/KEY: CDS
247 <222> LOCATION: (1)...(5427)
249 <400> SEQUENCE: 11
250 ttg gag cac agt ggg att gga aga atc aaa gag cag agt gcc cgc atg      48
251 Leu Glu His Ser Gly Ile Gly Arg Ile Lys Glu Gln Ser Ala Arg Met
252 1          5                      10                      15
254 ctg ggg cac ctg gtc tcc aat gcc ccc cga ctc atc cgc ccc tac atg      96
255 Leu Gly His Leu Val Ser Asn Ala Pro Arg Leu Ile Arg Pro Tyr Met

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256	20	25	30	
258	gag cct att ctg aag gca tta att ttg aaa ctg aaa gat cca gac cct	144		
259	Glu Pro Ile Leu Lys Ala Leu Ile Leu Lys Leu Lys Asp Pro Asp Pro			
260	35 40 45			
262	gat cca aac cca ggt gtg atc aat aat gtc ctg gca aca ata gga gaa	192		
263	Asp Pro Asn Pro Gly Val Ile Asn Asn Val Leu Ala Thr Ile Gly Glu			
264	50 55 60			
266	ttg gca cag gtt agt ggc ctg gaa atg agg aaa tgg gtt gat gaa ctt	240		
267	Leu Ala Gln Val Ser Gly Leu Glu Met Arg Lys Trp Val Asp Glu Leu			
268	65 70 75 80			
270	ttt att atc atc atg gac atg ctc cag gat tcc tct ttg ttg gcc aaa	288		
271	Phe Ile Ile Ile Met Asp Met Leu Gln Asp Ser Ser Leu Leu Ala Lys			
272	85 90 95			
274	agg cag gtg gct ctg tgg acc ctg gga cag ttg gtg gcc agc act ggc	336		
275	Arg Gln Val Ala Leu Trp Thr Leu Gly Gln Leu Val Ala Ser Thr Gly			
276	100 105 110			
278	tat gta gta gag ccc tac agg aag tac cct act ttg ctt gag gtg cta	384		
279	Tyr Val Val Glu Pro Tyr Arg Lys Tyr Pro Thr Leu Leu Glu Val Leu			
280	115 120 125			
282	ctg aat ttt ctg aag act gag cag aac cag ggt aca cgc aga gag gcc	432		
283	Leu Asn Phe Leu Lys Thr Glu Gln Asn Gln Gly Thr Arg Arg Glu Ala			
284	130 135 140			
286	atc cgt gtg tta ggg ctt tta ggg gct ttg gat cct tac aag cac aaa	480		
287	Ile Arg Val Leu Gly Leu Leu Gly Ala Leu Asp Pro Tyr Lys His Lys			
288	145 150 155 160			
290	gtg aac att ggc atg ata gac cag tcc cgg gat gcc tct gct gtc agc	528		
291	Val Asn Ile Gly Met Ile Asp Gln Ser Arg Asp Ala Ser Ala Val Ser			
292	165 170 175			
294	ctg tca gaa tcc aag tca agt cag gat tcc tct gac tat agc act agt	576		
295	Leu Ser Glu Ser Lys Ser Ser Gln Asp Ser Ser Asp Tyr Ser Thr Ser			
296	180 185 190			
298	gaa atg ctg gtc aac atg gga aac ttg cct ctg gat gag ttc tac cca	624		
299	Glu Met Leu Val Asn Met Gly Asn Leu Pro Leu Asp Glu Phe Tyr Pro			
300	195 200 205			
302	gct gtg tcc atg gtg gcc ctg atg cgg atc ttc cga gac cag tca ctc	672		
303	Ala Val Ser Met Val Ala Leu Met Arg Ile Phe Arg Asp Gln Ser Leu			
304	210 215 220			
306	tct cat cat cac acc atg gtt gtc cag gcc atc acc ttc atc ttc aag	720		
307	Ser His His His Thr Met Val Val Gln Ala Ile Thr Phe Ile Phe Lys			
308	225 230 235 240			
310	tcc ctg gga ctc aaa tgt gtg cag ttc ctg ccc cag gtc atg ccc acg	768		
311	Ser Leu Gly Leu Lys Cys Val Gln Phe Leu Pro Gln Val Met Pro Thr			
312	245 250 255			
314	ttc ctt aat gtc att cga gtc tgt gat ggg gcc atc cgg gaa ttt ttg	816		
315	Phe Leu Asn Val Ile Arg Val Cys Asp Gly Ala Ile Arg Glu Phe Leu			
316	260 265 270			
318	ttc cag cag ctg gga atg ttg gtg tcc ttt gtg aag agc cac atc aga	864		
319	Phe Gln Gln Leu Gly Met Leu Val Ser Phe Val Lys Ser His Ile Arg			
320	275 280 285			

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/517,491B

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:19; N Pos. 59,64,72,74,89,94,101,137,158,175,190,201,207,210,213,218
Seq#:19; N Pos. 234,243,257,283,286,289,292,314,325,328,335,352,361,380,384
Seq#:19; N Pos. 390,393,403,411,413,427,432,435,440,443,450,452,460,465,480
Seq#:19; N Pos. 482,486,492,515
Seq#:23; N Pos. 27,373,443,461,483,485,507,583,588,593,605,606,607,612,624
Seq#:23; N Pos. 625,626,627,628,630,631,632,635,639,646,652,659,661
Seq#:24; Xaa Pos. 105
Seq#:25; N Pos. 112,148,158,171,178,182,191,194,203,204
Seq#:29; N Pos. 3,9,15
Seq#:30; N Pos. 3,6,21

VERIFICATION SUMMARY

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Input Set : A:\ABPI-P06-036.TXT

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L:1157 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:19
L:1158 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
M:341 Repeated in SeqNo=19
L:1214 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:0
M:341 Repeated in SeqNo=23
L:1250 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:96
L:1264 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1268 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:25
L:1270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:60
M:341 Repeated in SeqNo=25
L:1312 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1316 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:29
L:1317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:0
L:1327 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1331 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30
L:1332 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0